

44

SEQUENCE LISTING



<110> TILG, YVONNE  
ELKMANN, BERND  
EGGELING, LOTHAR  
SAHM, HERMANN  
MOCKEL, BETTINA

<120> PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY  
FERMENTATION AND NUCLEOTIDE SEQUENCES CODING FOR THE  
accDA GENE

<130> 21123-284139-MAS

<140> 10/024,370  
<141> 2001-12-21

<150> 09/362,899  
<151> 1999-07-29

<150> DE 199 24 365.4  
<151> 1999-07-29

<160> 3

<170> PatentIn Ver. 2.1

<210> 1  
<211> 2123  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> gene  
<222> (508) .. (1980)  
<223> accDA

<400> 1  
ctcgagcggg agtcggtgat cggccactct ctaagcaatg ccggctttaa aataaagcaa 60  
cttatatggt tctcaccaca tctggccgac gaccacgaag tatgttgctg atcacagcta 120  
aacgtgtgaa tgtgaagtta cctaactcac attgcaatgc gatagcgatt tggaaaactc 180  
actcccccca atatcttaac ttaaacttaa aagtagtggt ttacctgcat ttataaaaagt 240  
tcccgatcta cccctctttt accccgaaat accccttttg caaagattgc aaacacaaca 300  
gtgcaatagt taacgggctt cacacgtcac cattctgtcc ggtttttaggc tatgttcggg 360  
acgtctaggg aaaaagtagt tttgtgagat gaaacgcata atccgtcatt ttttacgcaa 420  
tcgatagcct aaattgggct tagatcttcc gcctctaaat aggtatgcag agacattcga 480  
attaattaac aaagccattt ttcggccgtg gagaagcggt ttccgactat ggtgtggggc 540  
atggaacaca cttcagcatt gacgctcata gactcgggtt tggaccctga cagcttcatt 600  
tcttggaatg aaactcccc aatagacaac ctcaatcaag gctatgcaga gaccttggag 660  
cgggctcgaa gcaaggccaa atgcgatgaa tcggtaatta ctggagaagg caccgtggag 720  
ggcattccgg tagccgttat tttgtccgat ttttccttcc tcggcgggtt tttgggacag 780  
gtcgcgtcgg tgcgcatcat gaaggcgatt caccgcgcca cagagctgaa actcccactg 840  
ctggtctccc ctgcttccgg tgggtgcgcgc atgcaggaag acaatcgagc ttttgtcatg 900  
atgggtgtcca taaccgcggc tgtgcagcgt caccgcgagg cgcatttgcc gttcctgggtg 960  
tatttgcgca atcccacgat ggggtggcgcc atggcctcgt ggggttcacg tgggcatctc 1020  
acttttgcgg aaccgcggcg gcagataggt ttcttggtgc ctgcgctggt ggagttaacc 1080  
actgggcatg cgcttccaga cgggtgtgcag caggcggaga atttggtgaa aactgggtgtg 1140  
attgatggaa ttgtgtcgcc actccaattg cgtgcagcgg tggcaaaaac cctcaagggt 1200

```

attcagccgg tagaggcaac ggatcgtttt tctccaacaa ctccctggcgt ggcacttccg 1260
gtgatggagg cgattgcgcg ttctcgtgac ccgcagaggc ctggaatcgg ggagattatg 1320
gaaacgttgg gggcagacgt cgtcaagctt tctggtgcgc gtgctggcgc attgagcccg 1380
gctgtgcgcg ttgccctggc gcgcacgcgg ggccggcccg tgggtgctgat tgggcaggat 1440
cgccgcttca cgcttggggc gcaggagctg cgttttgcgc gtcgtggcat ttcgctggcg 1500
cgcgagctaa acctgccgat cgtgtccatc atcgacacct ccggcgccga attgtcgcag 1560
gcggctgagg agctcggcat cgcaagctcg attgcgcgca ccttgtccaa gcttatcgac 1620
gctccccctc ccaccgtttc ggtcattatt ggtcaggggc ttggcggtgg ccgctggcc 1680
atgctgcccc ccgatctggg ctacgcggcc gaaaacgcgt ggctgtccgc attgccacca 1740
gagggcgctt cggccatcct cttccgcgac accaaccacg ccgcggaaat catagagcga 1800
caaggcgtgc aggcgcacgc acttttaagc caagggttta tcgacgggat cgtcgccgaa 1860
accgagcact ttgttgaaga aattctcggc acaatcagca acgccctctc cgaattggat 1920
aacaatccgg agagggcggg acgcgacagt cgcttcacac gatttgagcg tttagcgcag 1980
taaagaaaat tatgcgctga tcaaatcgat gatgaacacc aggggtacggc cagacagtgg 2040
gtggccggaa ccctcagggc cgtaagcagc ctctggcgga atggtcagct gacgacgtcc 2100
gccgaccttc atgcttgaa ttc 2123

```

<210> 2

<211> 1473

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1473)

<223> accDA

<400> 2

```

gtg gag aag cgt ttt ccg act atg gtg tgg ggc atg gaa cac act tca 48
Val Glu Lys Arg Phe Pro Thr Met Val Trp Gly Met Glu His Thr Ser
1 5 10 15

gca ttg acg ctc ata gac tcg gtt ttg gac cct gac agc ttc att tct 96
Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp Ser Phe Ile Ser
20 25 30

tgg aat gaa act ccc caa tat gac aac ctc aat caa ggc tat gca gag 144
Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln Gly Tyr Ala Glu
35 40 45

acc ttg gag cgg gct cga agc aag gcc aaa tgc gat gaa tcg gta att 192
Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp Glu Ser Val Ile
50 55 60

act gga gaa ggc acc gtg gag ggc att ccg gta gcc gtt att ttg tcc 240
Thr Gly Glu Gly Thr Val Glu Gly Ile Pro Val Ala Val Ile Leu Ser
65 70 75 80

gat ttt tcc ttc ctc ggc ggt tct ttg ggc acg gtc gcg tcg gtg cgc 288
Asp Phe Ser Phe Leu Gly Gly Ser Leu Gly Thr Val Ala Ser Val Arg
85 90 95

atc atg aag gcg att cac cgc gcc aca gag ctg aaa ctc cca ctg ctg 336
Ile Met Lys Ala Ile His Arg Ala Thr Glu Leu Lys Leu Pro Leu Leu
100 105 110

```

gtc tcc cct gct tcc ggt ggt gcg cgc atg cag gaa gac aat cga gct	384
Val Ser Pro Ala Ser Gly Gly Ala Arg Met Gln Glu Asp Asn Arg Ala	
115 120 125	
ttt gtc atg atg gtg tcc ata acc gcg gct gtg cag cgt cac cgc gag	432
Phe Val Met Met Val Ser Ile Thr Ala Ala Val Gln Arg His Arg Glu	
130 135 140	
gcg cat ttg ccg ttc ctg gtg tat ttg cgc aat ccc acg atg ggt ggc	480
Ala His Leu Pro Phe Leu Val Tyr Leu Arg Asn Pro Thr Met Gly Gly	
145 150 155 160	
gcc atg gcc tcg tgg ggt tca tct ggg cat ctc act ttt gcg gaa ccc	528
Ala Met Ala Ser Trp Gly Ser Ser Gly His Leu Thr Phe Ala Glu Pro	
165 170 175	
ggc gcg cag ata ggt ttc ctg ggt cct cgc gtg gtg gag tta acc act	576
Gly Ala Gln Ile Gly Phe Leu Gly Pro Arg Val Val Glu Leu Thr Thr	
180 185 190	
ggg cat gcg ctt cca gac ggt gtg cag cag gcg gag aat ttg gtg aaa	624
Gly His Ala Leu Pro Asp Gly Val Gln Gln Ala Glu Asn Leu Val Lys	
195 200 205	
act ggt gtg att gat gga att gtg tcg cca ctc caa ttg cgt gca gcg	672
Thr Gly Val Ile Asp Gly Ile Val Ser Pro Leu Gln Leu Arg Ala Ala	
210 215 220	
gtg gca aaa acc ctc aag gtt att cag ccg gta gag gca acg gat cgt	720
Val Ala Lys Thr Leu Lys Val Ile Gln Pro Val Glu Ala Thr Asp Arg	
225 230 235 240	
ttt tct cca aca act cct ggc gtg gca ctt ccg gtg atg gag gcg att	768
Phe Ser Pro Thr Thr Pro Gly Val Ala Leu Pro Val Met Glu Ala Ile	
245 250 255	
gcg cgt tct cgt gac ccg cag agg cct gga atc ggg gag att atg gaa	816
Ala Arg Ser Arg Asp Pro Gln Arg Pro Gly Ile Gly Glu Ile Met Glu	
260 265 270	
acg ttg ggg gca gac gtc gtc aag ctt tct ggt gcg cgt gct ggc gca	864
Thr Leu Gly Ala Asp Val Val Lys Leu Ser Gly Ala Arg Ala Gly Ala	
275 280 285	
ttg agc ccg gct gtg cgc gtt gcc ctg gcg cgc atc ggg ggc cgg ccc	912
Leu Ser Pro Ala Val Arg Val Ala Leu Ala Arg Ile Gly Gly Arg Pro	
290 295 300	
gtg gtg ctg att ggg cag gat cgc cgc ttc acg ctt ggg ccg cag gag	960
Val Val Leu Ile Gly Gln Asp Arg Arg Phe Thr Leu Gly Pro Gln Glu	
305 310 315 320	
ctg cgt ttt gcg cgt cgt ggc att tcg ctg gcg cgc gag cta aac ctg	1008
Leu Arg Phe Ala Arg Arg Gly Ile Ser Leu Ala Arg Glu Leu Asn Leu	
325 330 335	

ccg atc gtg tcc atc atc gac acc tcc ggc gcc gaa ttg tgc cag gcg 1056  
 Pro Ile Val Ser Ile Ile Asp Thr Ser Gly Ala Glu Leu Ser Gln Ala  
 340 345 350

gct gag gag ctc ggc atc gca agc tgc att gcg cgc acc ttg tcc aag 1104  
 Ala Glu Glu Leu Gly Ile Ala Ser Ser Ile Ala Arg Thr Leu Ser Lys  
 355 360 365

ctt atc gac gct ccc ctc ccc acc gtt tgc gtc att att ggt cag gcg 1152  
 Leu Ile Asp Ala Pro Leu Pro Thr Val Ser Val Ile Ile Gly Gln Gly  
 370 375 380

gtt ggc ggt ggc gcg ctg gcc atg ctg ccc gcc gat ctg gtc tac gcg 1200  
 Val Gly Gly Gly Ala Leu Ala Met Leu Pro Ala Asp Leu Val Tyr Ala  
 385 390 395 400

gcc gaa aac gcg tgg ctg tcc gca ttg cca cca gag ggc gcc tgc gcc 1248  
 Ala Glu Asn Ala Trp Leu Ser Ala Leu Pro Pro Glu Gly Ala Ser Ala  
 405 410 415

atc ctc ttc cgc gac acc aac cac gcc gcg gaa atc ata gag cga caa 1296  
 Ile Leu Phe Arg Asp Thr Asn His Ala Ala Glu Ile Ile Glu Arg Gln  
 420 425 430

ggc gtg cag gcg cac gca ctt tta agc caa ggg ctt atc gac ggg atc 1344  
 Gly Val Gln Ala His Ala Leu Leu Ser Gln Gly Leu Ile Asp Gly Ile  
 435 440 445

gtc gcc gaa acc gag cac ttt gtt gaa gaa att ctc ggc aca atc agc 1392  
 Val Ala Glu Thr Glu His Phe Val Glu Glu Ile Leu Gly Thr Ile Ser  
 450 455 460

aac gcc ctc tcc gaa ttg gat aac aat ccg gag agg gcg gga cgc gac 1440  
 Asn Ala Leu Ser Glu Leu Asp Asn Asn Pro Glu Arg Ala Gly Arg Asp  
 465 470 475 480

agt cgc ttc aca cga ttt gag cgt tta gcg cag 1473  
 Ser Arg Phe Thr Arg Phe Glu Arg Leu Ala Gln  
 485 490

<210> 3

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 3

Val Glu Lys Arg Phe Pro Thr Met Val Trp Gly Met Glu His Thr Ser  
 1 5 10 15

Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp Ser Phe Ile Ser  
 20 25 30

Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln Gly Tyr Ala Glu  
 35 40 45

Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp Glu Ser Val Ile  
 50 55 60

Thr	Gly	Glu	Gly	Thr	Val	Glu	Gly	Ile	Pro	Val	Ala	Val	Ile	Leu	Ser	65	70	75	80
Asp	Phe	Ser	Phe	Leu	Gly	Gly	Ser	Leu	Gly	Thr	Val	Ala	Ser	Val	Arg	85	90	95	
Ile	Met	Lys	Ala	Ile	His	Arg	Ala	Thr	Glu	Leu	Lys	Leu	Pro	Leu	Leu	100	105	110	
Val	Ser	Pro	Ala	Ser	Gly	Gly	Ala	Arg	Met	Gln	Glu	Asp	Asn	Arg	Ala	115	120	125	
Phe	Val	Met	Met	Val	Ser	Ile	Thr	Ala	Ala	Val	Gln	Arg	His	Arg	Glu	130	135	140	
Ala	His	Leu	Pro	Phe	Leu	Val	Tyr	Leu	Arg	Asn	Pro	Thr	Met	Gly	Gly	145	150	155	160
Ala	Met	Ala	Ser	Trp	Gly	Ser	Ser	Gly	His	Leu	Thr	Phe	Ala	Glu	Pro	165	170	175	
Gly	Ala	Gln	Ile	Gly	Phe	Leu	Gly	Pro	Arg	Val	Val	Glu	Leu	Thr	Thr	180	185	190	
Gly	His	Ala	Leu	Pro	Asp	Gly	Val	Gln	Gln	Ala	Glu	Asn	Leu	Val	Lys	195	200	205	
Thr	Gly	Val	Ile	Asp	Gly	Ile	Val	Ser	Pro	Leu	Gln	Leu	Arg	Ala	Ala	210	215	220	
Val	Ala	Lys	Thr	Leu	Lys	Val	Ile	Gln	Pro	Val	Glu	Ala	Thr	Asp	Arg	225	230	235	240
Phe	Ser	Pro	Thr	Thr	Pro	Gly	Val	Ala	Leu	Pro	Val	Met	Glu	Ala	Ile	245	250	255	
Ala	Arg	Ser	Arg	Asp	Pro	Gln	Arg	Pro	Gly	Ile	Gly	Glu	Ile	Met	Glu	260	265	270	
Thr	Leu	Gly	Ala	Asp	Val	Val	Lys	Leu	Ser	Gly	Ala	Arg	Ala	Gly	Ala	275	280	285	
Leu	Ser	Pro	Ala	Val	Arg	Val	Ala	Leu	Ala	Arg	Ile	Gly	Gly	Arg	Pro	290	295	300	
Val	Val	Leu	Ile	Gly	Gln	Asp	Arg	Arg	Phe	Thr	Leu	Gly	Pro	Gln	Glu	305	310	315	320
Leu	Arg	Phe	Ala	Arg	Arg	Gly	Ile	Ser	Leu	Ala	Arg	Glu	Leu	Asn	Leu	325	330	335	
Pro	Ile	Val	Ser	Ile	Ile	Asp	Thr	Ser	Gly	Ala	Glu	Leu	Ser	Gln	Ala	340	345	350	
Ala	Glu	Glu	Leu	Gly	Ile	Ala	Ser	Ser	Ile	Ala	Arg	Thr	Leu	Ser	Lys	355	360	365	

Leu	Ile	Asp	Ala	Pro	Leu	Pro	Thr	Val	Ser	Val	Ile	Ile	Gly	Gln	Gly	
370						375					380					
Val	Gly	Gly	Gly	Ala	Leu	Ala	Met	Leu	Pro	Ala	Asp	Leu	Val	Tyr	Ala	
385					390					395					400	
Ala	Glu	Asn	Ala	Trp	Leu	Ser	Ala	Leu	Pro	Pro	Glu	Gly	Ala	Ser	Ala	
				405					410					415		
Ile	Leu	Phe	Arg	Asp	Thr	Asn	His	Ala	Ala	Glu	Ile	Ile	Glu	Arg	Gln	
			420					425					430			
Gly	Val	Gln	Ala	His	Ala	Leu	Leu	Ser	Gln	Gly	Leu	Ile	Asp	Gly	Ile	
		435					440					445				
Val	Ala	Glu	Thr	Glu	His	Phe	Val	Glu	Glu	Ile	Leu	Gly	Thr	Ile	Ser	
	450					455					460					
Asn	Ala	Leu	Ser	Glu	Leu	Asp	Asn	Asn	Pro	Glu	Arg	Ala	Gly	Arg	Asp	
465					470					475					480	
Ser	Arg	Phe	Thr	Arg	Phe	Glu	Arg	Leu	Ala	Gln						
				485					490							